Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

Claims 1-22 (cancelled)

23. (New) A method of screening for altered immunogenicity of a target protein, said method comprising:

a) inputting a target protein backbone structure with variable residue positions into a computer;

b) applying, in any order:

i) at least one computational protein design algorithm using at least two scoring functions;

ii) an immunogenicity filter that creates at least one immunogenic sequence of variable residue positions, said immunogenic sequence selected from the group consisting of sequences that bind to MHC class I molecules, sequences that bind to MHC class II molecules, sequences that bind to T cell epitopes, sequences that bind to B cell epitopes, and specific cleavage motifs for antigen processing and presentation;

c) synthesizing a plurality of variant proteins each comprising at least one of said immunogenic sequences; and,

f) selecting a variant protein with altered immunogenicity.

24. (New) A method of screening for altered immunogenicity of a target protein, said method comprising:

a) inputting a target protein backbone structure with variable residue positions into a computer;

b) applying, in any order:

i) at least one computational protein design algorithm using at least two scoring functions;

ii) an immunogenicity filter that removes at least one immunogenic sequence of said target protein by creating at least one variant immunogenic sequence, said immunogenic sequence selected from the group consisting of sequences that bind to MHC class I molecules, sequences that bind to MHC class II molecules, sequences that bind to T cell epitopes, sequences that bind to B cell epitopes, and specific cleavage motifs for antigen processing and presentation;

c) synthesizing a plurality of variant proteins each comprising at least one of said variant immunogenic sequences; and,

f) selecting a variant protein with altered immunogenicity.

25. (New) A method according to claim 23 wherein at least one MHC class I molecule binding sequence is created in a variant protein.

26. (New) A method according to claim 23 wherein a plurality of MHC class I molecule binding sequences are created in a variant protein.

27. (New) A method according to claim 23 or 24 wherein said cleavage motif is a proteasomal cleavage site.

28. (New) A method according to claim 23 or 24 wherein at least one cleavage motif is altered in a variant protein.

29. (New) A method according to claim 28 wherein said cleavage motif is selected from the group consisting of a cleavage motif for catheptsin B, cathepsin D, cathepsin E, cathepsin L and asparaginyl endopeptidase.

30. (New) A method according to claim 28 wherein at least one cleavage motif is added.

31. (New) A method according to claim 28 wherein at least one cleavage motif is removed.

32. (New) A method according to claim 23 or 24 wherein said scoring functions are selected from the group consisting of a Van der Waal's potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.